

16/37

atg aca tcg ccc cag cta gag tgg act ctg cag acc ctt ctg gag cag Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln 1 5 10 15	48
ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe 20 25 30	96
ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu 35 40 45	144
gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu 50 55 60	192
aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu 65 70 75 80	240
acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln 85 90 95	288
gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser 100 105 110	336
gag tta gca aag cca ggt gaa aag gaa gga tgg aga aat tca atg gag Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu 115 120 125	384
aaa caa tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp 130 135 140	432
aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe 145 150 155 160	480
ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu 165 170 175	528
cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met 180 185 190	576
ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe 195 200 205	624

Fig. 1A

tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca		672
Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala		
210	215	220
 gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc		720
Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser		
225	230	235
240		
 atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat		768
Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp		
245	250	255
 gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac		816
Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp		
260	265	270
 tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag		864
Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys		
275	280	285
 agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg		912
Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg		
290	295	300
 gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg		960
Ala Leu Arg Asp Leu Gln Leu Ala Gln Gln Pro Ile Tyr Ile Arg		
305	310	315
320		
 gtg gag ggc ttc ctg gag gac agg agg gcc tat ttc ctg aga cac		1008
Val Glu Gly Phe Leu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His		
325	330	335
 ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc		1056
Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser		
340	345	350
 aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att		1104
Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile		
355	360	365
 gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg		1152
Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro		
370	375	380
 gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct		1200
Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro		
385	390	395
400		
 cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag		1248
Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu		
405	410	415

Fig. 1B

gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu 420 425 430	1296
gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac tcc Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser 435 440 445	1344
ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac gcc Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala 450 455 460	1392
ctg gag aag gag gag gag gac agg gac ggc cac gcc tgg gac att Leu Glu Lys Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile 465 470 475 480	1440
ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac ccc Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro 485 490 495	1488
gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag aag Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys 500 505 510	1536
aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg gac Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp 515 520 525	1584
atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat aag Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys 530 535 540	1632
ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat gag Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu 545 550 555 560	1680
tct cag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag gaa Ser Gln Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu 565 570 575	1728
att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc ttc Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe 580 585 590	1776
agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta gca Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala 595 600 605	1824
aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att gaa Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu 610 615 620	1872

Fig. 1C

ttt gaa agc tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser 625	630	635	640	1920
ttc ctg agt gac tct tct gtg cggtt gac cac gta acc acc cgt Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg 645	650		655	1968
agc acc tgt cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp 660	665		670	2016
acc gcg tac cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu 675	680		685	2064
acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met 690	695		700	2112
ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr 705	710	715	720	2160
ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe 725	730		735	2208
ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser 740	745		750	2256
gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met 755	760		765	2304
aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg 770	775		780	2352
ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser 785	790	795	800	2400
aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr 805	810		815	2448
ggg gtg aag ttt ctg t Gly Val Lys Phe Leu 820				2464

Fig. 1D

Qas  
Holo  
cut  
TH  
ins

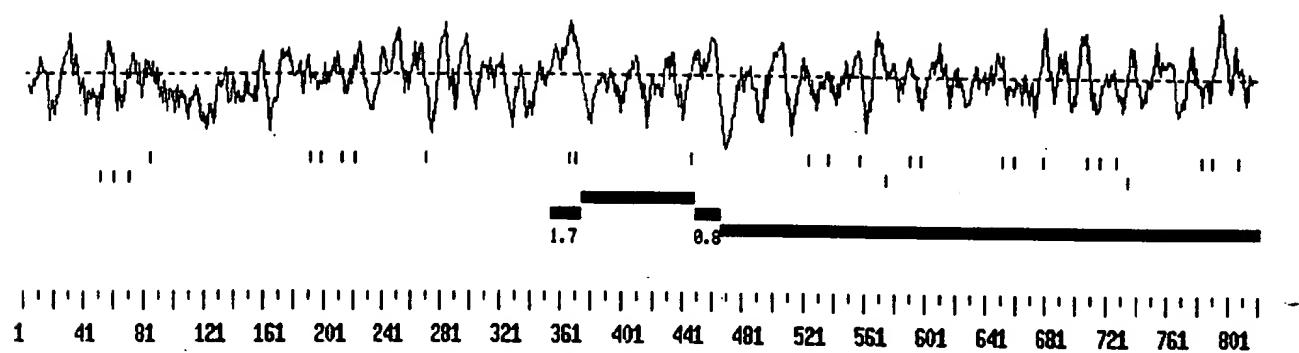


Fig.2

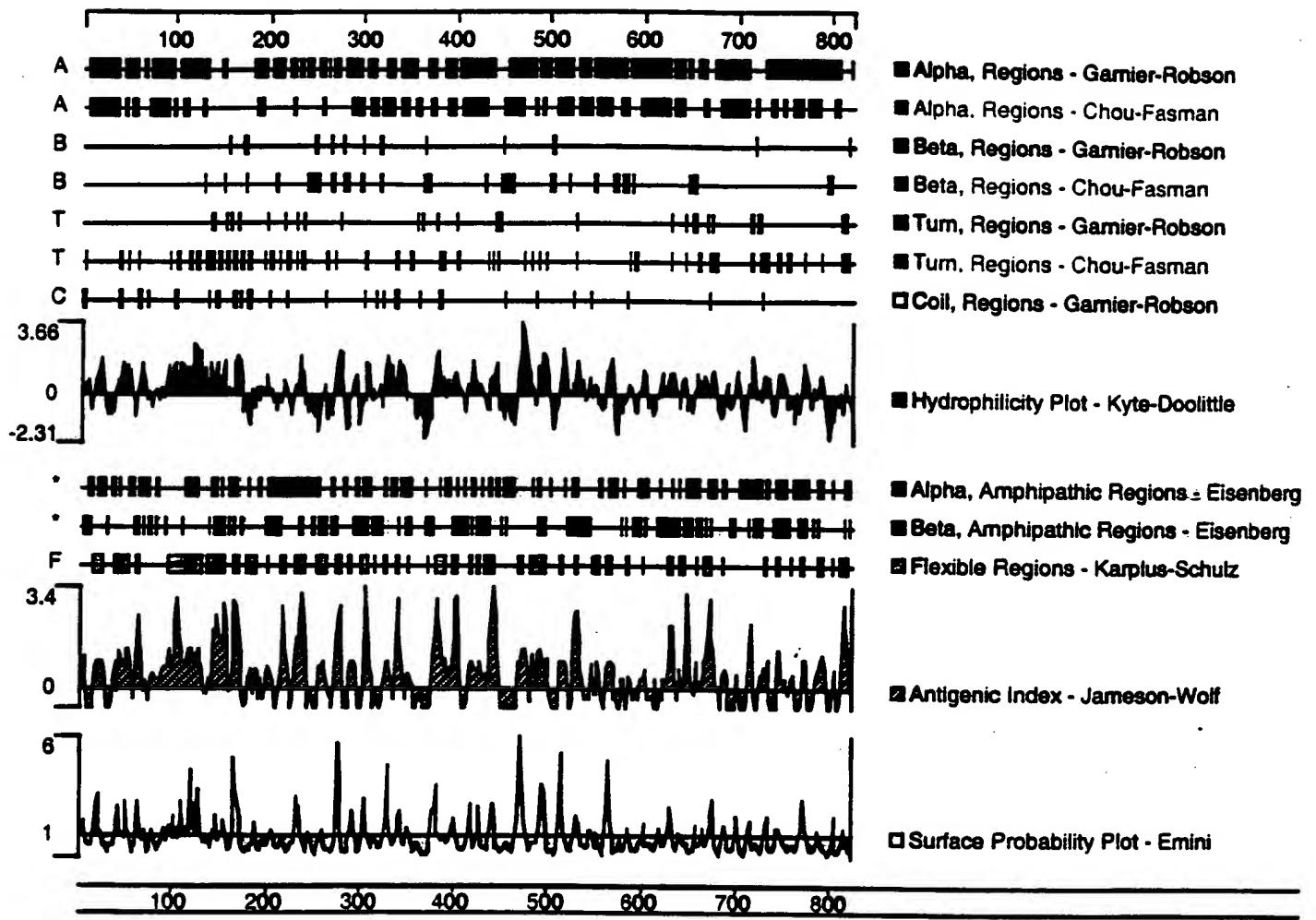


Fig. 3

NB-ARC: domain 1 of 1, from 176 to 190: score 11.4, E = 0.033  
SEQ ID No:9 \*->ivGMGGiGKTTLakq<-\*  
++G++G+GKTTLak+  
NBS-2 176 LHGPAGVGKTTLAKK 190

Fig. 4A

LRR\_RI\_2: domain 1 of 2, from 743 to 770: score 13.4, E = 0.57  
SEQ ID No:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
n+sL+ L+Ls N 1 deGa+ L ++ +  
NBS-2 743 NQSLKHLRLSANVLLDEGAMLLYKTMTR 770

Fig. 4B

LRR\_RI\_2: domain 2 of 2, from 772 to 799: score 18.2, E = 0.12  
SEQ ID No:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
++ L+ L+L+n+ 1+++ ++ La++L  
NBS-2 772 KHFLQMLSENCRLTEASCKDLAAVLVV 799

Fig. 4C

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	48
1 5 10 15	
 aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	96
20 25 30	
 aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	144
35 40 45	
 aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	192
50 55 60	
 ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	240
65 70 75 80	
 ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	288
85 90 95	
 caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	336
100 105 110	
 gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	384
115 120 125	
 ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	432
130 135 140	
 tcg tac gtc gtt cac ctc act gct cac gaa ata aac cag atg acc aac Ser Tyr Val Val His Leu Thr Ala His Glu Ile Asn Gln Met Thr Asn	480
145 150 155 160	
 agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	528
165 170 175	
 ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc atc ctc Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	576
180 185 190	
 gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	624
195 200 205	

Fig. 5A

ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc		672	
Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val			
210	215	220	
agt ttg ctg aag aga aaa atg gct cca ggc tgc tgg ttc ctc atc tcc		720	
Ser Leu Leu Lys Arg Lys Met Ala Pro Gly Cys Trp Phe Leu Ile Ser			
225	230	235	240
tca agg ccc aca cgt ggg aat aat gta aaa acg ttc ttg aaa gag gta		768	
Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu Val			
245	250	255	
gat tgc tgc acg acc ttg cag ctg tcg aat ggg aag agg gag ata tat		816	
Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Ile Tyr			
260	265	270	
ttt aac tct ttc ttt aaa gac cgc cag agg gcg tcg gca gcc ctc cag		864	
Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu Gln			
275	280	285	
ctt gta cat gag gat gaa ata ctc gtg ggt ctg tgc cga gtc gcc atc		912	
Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala Ile			
290	295	300	
tta tgc tgg atc acg tgt act gtc ctg aag cgg cag atg gac aag ggg		960	
Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys Gly			
305	310	315	320
cgt gac ttc cag ctc tgc tgc caa aca ccc act gat cta cat gcc cac		1008	
Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala His			
325	330	335	
ttt ctt gct gat gcg ttg aca tca gag gct gga ctt act gcc aat cag		1056	
Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn Gln			
340	345	350	
tat cac cta ggt ctc cta aaa cgt ctg tgt ttg ctg gct gca gga gga		1104	
Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly Gly			
355	360	365	
ctg ttt ctg agc acc ctg aat ttc agt ggt gaa gac ctc aga tgt gtt		1152	
Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys Val			
370	375	380	
ggg ttt act gag gct gat gtc tct gtg ttg cag gcc gcg aat att ctt		1200	
Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile Leu			
385	390	395	400
ttg ccg agc aac act cat aaa gac cgt tac aag ttc ata cac ttg aac		1248	
Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu Asn			
405	410	415	

Fig. 5B

gtc cag gag ttt tgt aca gcc att gca ttt ctg atg gca gta ccc aac Val Gln Glu Phe Cys Thr Ala Ile Ala Phe Leu Met Ala Val Pro Asn 420                          425                          430	1296
tat ctg atc ccc tca ggc agc aga gag tat aaa gag aag aga gaa caa Tyr Leu Ile Pro Ser Gly Ser Arg Glu Tyr Lys Glu Lys Arg Glu Gln 435                          440                          445	1344
tac tct gac ttt aatcaa gtg ttt act ttc att ttt ggt ctt cta aat Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn 450                          455                          460	1392
gca aac agg aga aag att ctt gag aca tcc ttt gga tac cag cta ccg Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro 465                          470                          475                          480	1440
atg gta gac agc ttc aag tgg tac tcg gtg gga tac atg aaa cat ttg Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu 485                          490                          495	1488
gac cgt gac ccg gaa aag ttg acg cac cat atg cct ttg ttt tac tgt Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys 500                          505                          510	1536
ctc tat gag aat cgaa gaa gaa ttt gtg aag acg att gtg gat gct Leu Tyr Glu Asn Arg Glu Glu Phe Val Lys Thr Ile Val Asp Ala 515                          520                          525	1584
ctc atg gag gtt aca gtt tac ctt caa tca gac aag gat atg atg gtc Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val 530                          535                          540	1632
tca tta tac tgt ctg gat tac tgc tgt cac ctg agg aca ctt aag ttg Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu 545                          550                          555                          560	1680
agt gtt cag cgc atc ttt caa aac aaa gag cca ctt ata agg cca act Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr 565                          570                          575	1728
gct agt caa atg aag agc ctt gtc tac tgg aga gag atc tgc tct ctt Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu 580                          585                          590	1776
ttt tat aca atg gag agc ctc cgg gag ctg cat atc ttt gac aat gac Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp 595                          600                          605	1824
ctt aat ggt att tca gaa agg att ctg tct aaa gcc ctg gag cat tct Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser 610                          615                          620	1872

Fig. 5C

agc tgt aaa ctt cgc aca ctc aa  
Ser Cys Lys Leu Arg Thr Leu  
625                   630

1895

Fig. 5D

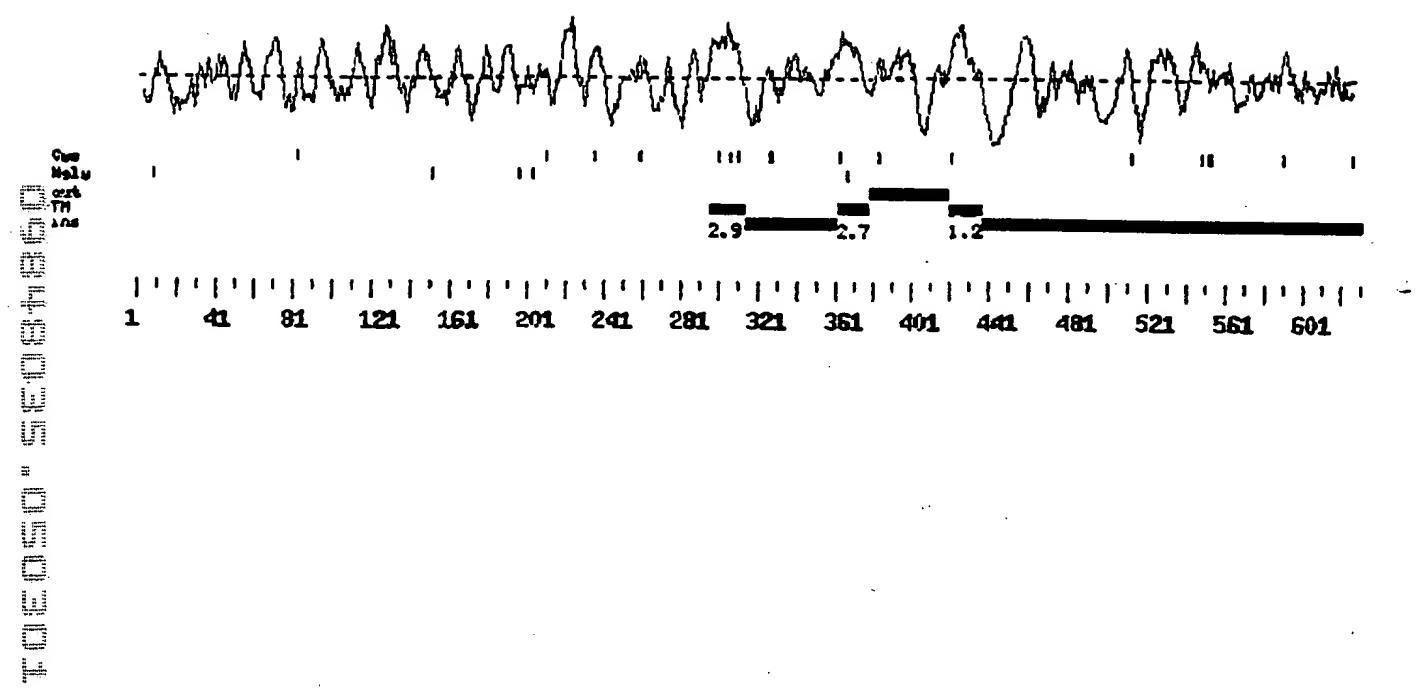


Fig. 6

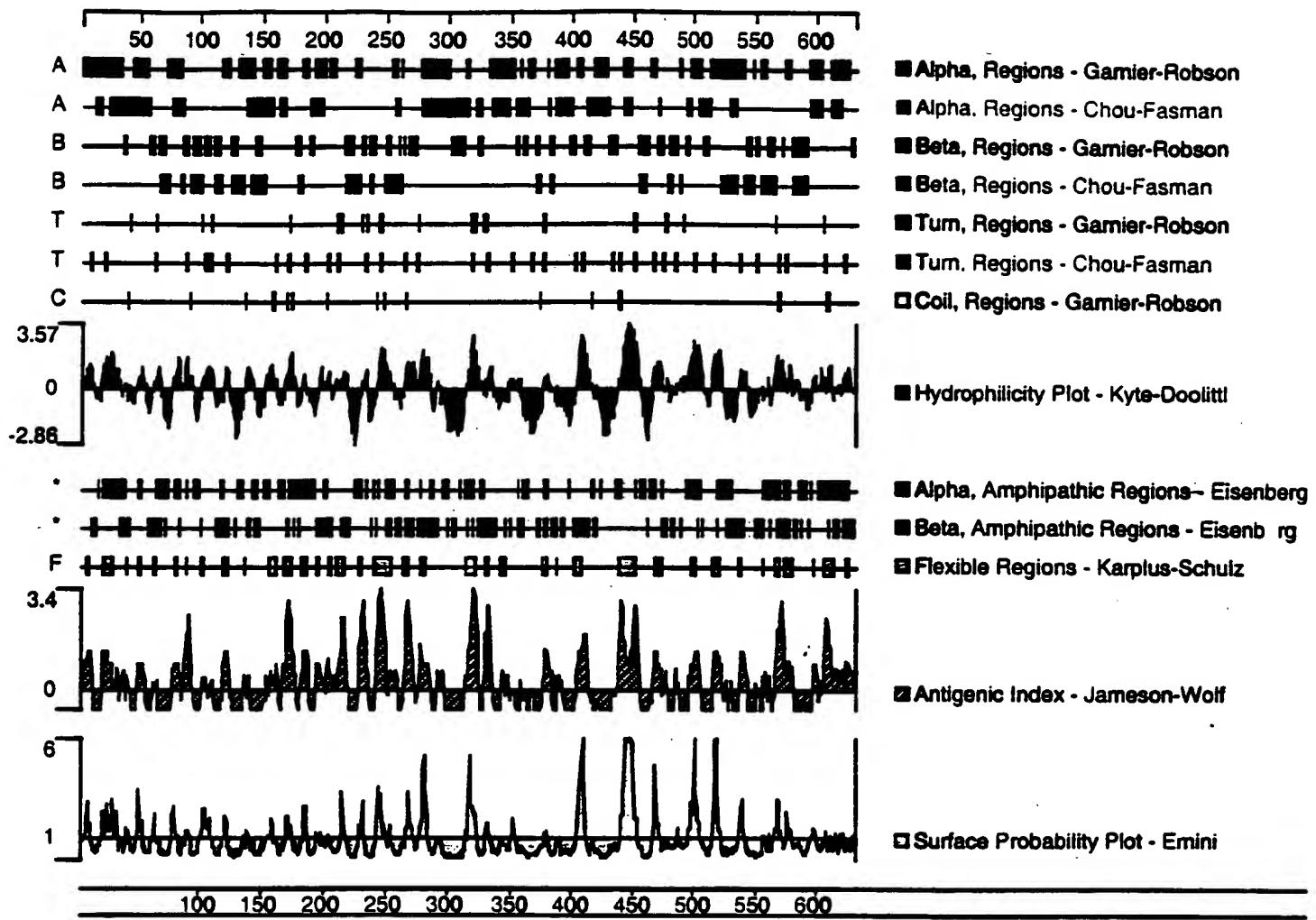


Fig. 7

LRR\_RI\_2: domain 1 of 1, from 596 to 623: score 11.0, E = 1.2  
SEQ ID No:10 \*->npsLreLdLenNk1gdeGaraLaalks<-\*  
\*\*SLreL++ \*N+1 r L++aL++  
NBS-3 596 MNSLRELHIFDNDLNGISERILSKALEH 623

Fig. 8

atg aag gct gaa cta ctg gag aca tgg gac aac atc agt tgg cct aaa Met Lys Ala Glu Leu Leu Glu Thr Trp Asp Asn Ile Ser Trp Pro Lys	48
1 5 10 15	
 gac cac gta tat atc cgt aat aca tca aag gac gaa cat gag gaa ctg Asp His Val Tyr Ile Arg Asn Thr Ser Lys Asp Glu His Glu Glu Leu	96
20 25 30	
 cag cgc cta ctg gat cct aat agg act aga gcc cag gcc cag acg ata Gln Arg Leu Leu Asp Pro Asn Arg Thr Arg Ala Gln Ala Gln Thr Ile	144
35 40 45	
 gtc ttg gtg ggg agg gca ggg gtt ggg aag acc acc ttg gca atg cag Val Leu Val Gly Arg Ala Gly Val Gly Lys Thr Thr Leu Ala Met Gln	192
50 55 60	
 gct atg ctg cac tgg gca aat gga gtt ctc ttt cag caa agg ttc tcc Ala Met Leu His Trp Ala Asn Gly Val Leu Phe Gln Gln Arg Phe Ser	240
65 70 75 80	
 tat gtt ttc tat ctc agc tgc cat aaa ata agg tac atg aag gaa act Tyr Val Phe Tyr Leu Ser Cys His Lys Ile Arg Tyr Met Lys Glu Thr	288
85 90 95	
 acc ttt gct gaa ttg att tct ttg gat tgg ccc gat ttt gat gcc ccc Thr Phe Ala Glu Leu Ile Ser Leu Asp Trp Pro Asp Phe Asp Ala Pro	336
100 105 110	
 att gaa gag ttc atg tct caa cca gag aag ctc ctg ttt att att gat Ile Glu Glu Phe Met Ser Gln Pro Glu Lys Leu Leu Phe Ile Ile Asp	384
115 120 125	
 ggc ttt gag gaa ata atc ata tct gag tca cgc tct gag agc ttg gat Gly Phe Glu Glu Ile Ile Ser Glu Ser Arg Ser Glu Ser Leu Asp	432
130 135 140	
 gat ggc tcg cca tgt aca gac tgg tac cag gag ctc cca gtg acc aaa Asp Gly Ser Pro Cys Thr Asp Trp Tyr Gln Glu Leu Pro Val Thr Lys	480
145 150 155 160	
 atc cta cac agc ttg ttg aag aaa gaa ttg gtt ccc ctg gct acc tta Ile Leu His Ser Leu Leu Lys Lys Glu Leu Val Pro Leu Ala Thr Leu	528
165 170 175	
 ctg atc acg atc aag acc tgg ttt gtg aga gat ctt aag gcc tca tta Leu Ile Thr Ile Lys Thr Trp Phe Val Arg Asp Leu Lys Ala Ser Leu	576
180 185 190	
 gtg aat cca tgc ttt gta caa att aca ggg ttc aca ggg gac gac cta Val Asn Pro Cys Phe Val Gln Ile Thr Gly Phe Thr Gly Asp Asp Leu	624
195 200 205	

Fig. 9A

Fig. 9B

ctg gaa gat act ttg cat tgt aaa ata tct ccc agg gta atg gag gaa Leu Glu Asp Thr Leu His Cys Lys Ile Ser Pro Arg Val Met Glu Glu	1296
420                                  425                                  430	
tta tta aag tgg gga gaa gag tta ggt aag gct gaa agt gcc tct ctc Leu Leu Lys Trp Gly Glu Glu Leu Gly Lys Ala Glu Ser Ala Ser Leu	1344
435                                  440                                  445	
caa ttt cac att cta cga ctt ttt cac tgc cta cac gag tcc cag gag Gln Phe His Ile Leu Arg Leu Phe His Cys Leu His Glu Ser Gln Glu	1392
450                                  455                                  460	
gaa gac ttc aca aag aag atg ttg ggt cgt atc ttt gaa gtt gac ctt Glu Asp Phe Thr Lys Lys Met Leu Gly Arg Ile Phe Glu Val Asp Leu	1440
465                                  470                                  475                                  480	
aat att ttg gag gac gaa gaa ctc caa gct tct tca ttt tgc cta aag Asn Ile Leu Glu Asp Glu Glu Leu Gln Ala Ser Ser Phe Cys Leu Lys	1488
485                                  490                                  495	
cac tgt aaa agg tta aat aag cta agg ctt tct gtt agc agt cac atc His Cys Lys Arg Leu Asn Lys Leu Arg Leu Ser Val Ser Ser His Ile	1536
500                                  505                                  510	
ctt gaa agg gac ttg gaa att ctg gag tga Leu Glu Arg Asp Leu Glu Ile Leu Glu	1566
515                                  520	

Fig. 9C

F0E090° 440000000000

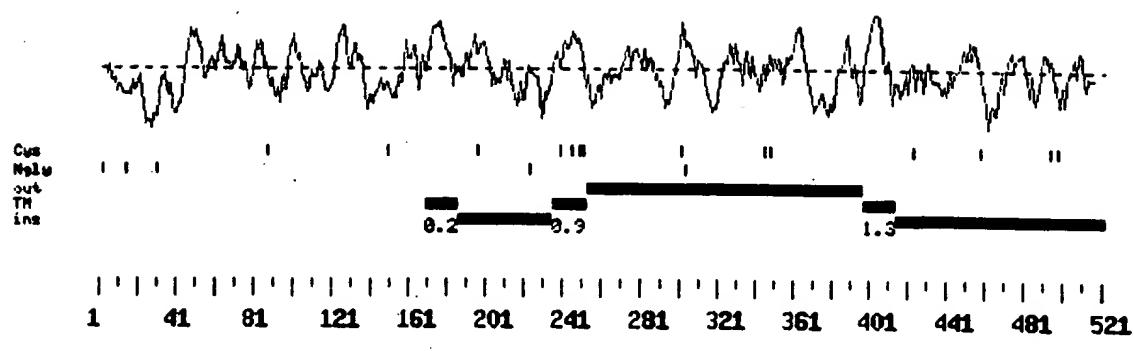


Fig. 10

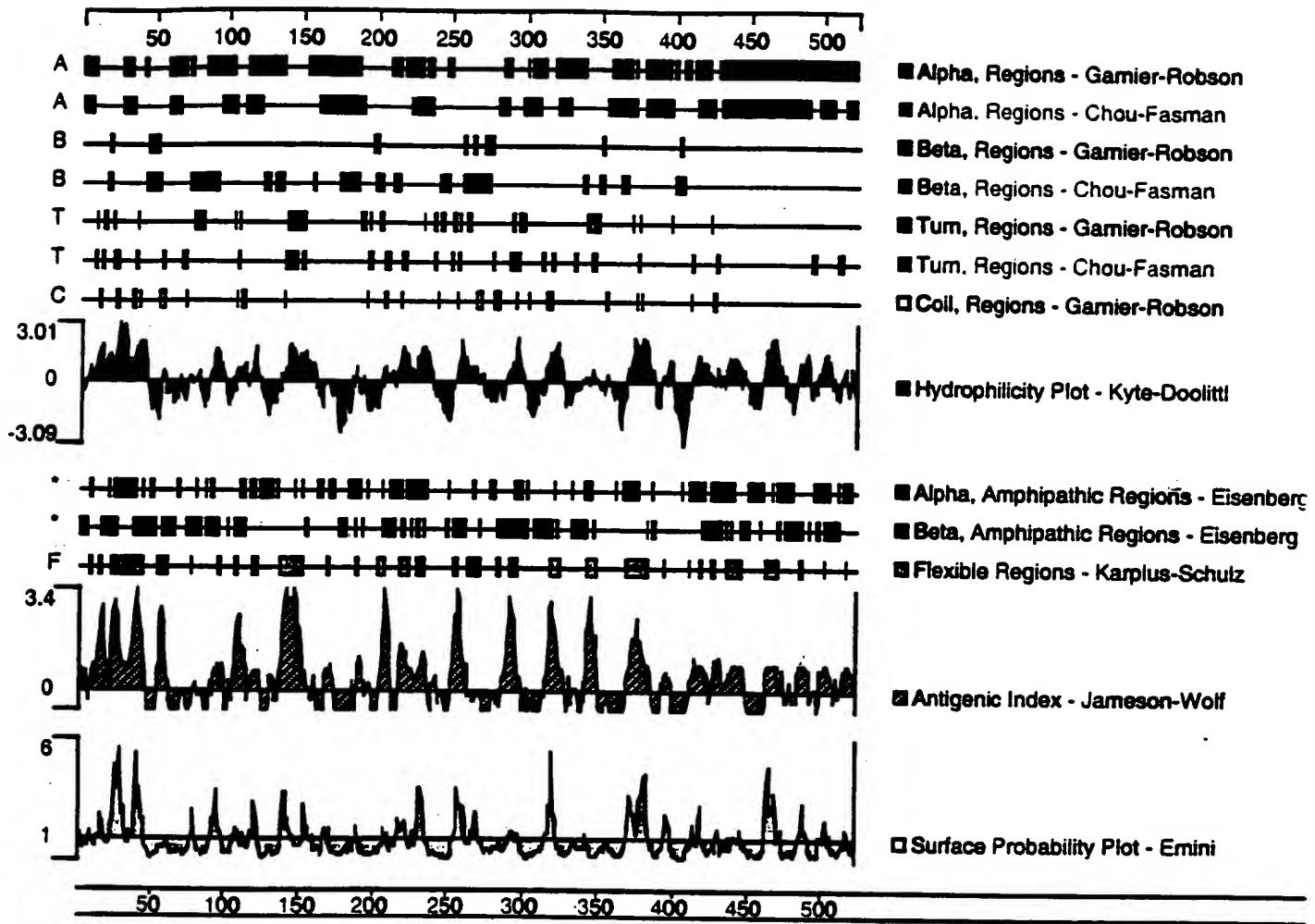


Fig. 11

TOE050 "GEM34860

NB-ARC: domain 1 of 1, from 50 to 79: score 9.4, E = 0.12  
SEQID No: 11 \*->ivGMGGIGKTTLakqiynedes..qevqrhf<-\*  
+vG++G+GKTTLa q+ +++++ ++q +F  
NBS-4 50 LVGRAGVGKTTLAMQAMLHWAngVLFQQRF 79

Fig. 1d

c agc cgc tta tgg tcc agc aag tct gtc act gag att cac cta tac ttt	49
Ser Arg Leu Trp Ser Ser Lys Ser Val Thr Glu Ile His Leu Tyr Phe	
1 5 10 15	
 gag gag gaa gtc aag caa gaa gaa tgt gac cat ttg gac cgc ctt ttt	97
Glu Glu Glu Val Lys Gln Glu Cys Asp His Leu Asp Arg Leu Phe	
20 25 30	
 gct ccc aag gaa gct ggg aaa cag cca cgt aca gtg atc att caa gga	145
Ala Pro Lys Glu Ala Gly Lys Gln Pro Arg Thr Val Ile Ile Gln Gly	
35 40 45	
 cca caa gga att gga aaa acg aca ctc ctg atg aag ctg atg atg gcc	193
Pro Gln Gly Ile Gly Lys Thr Thr Leu Leu Met Lys Leu Met Met Ala	
50 55 60	
 tgg tcg gac aac aag atc ttt cgg gat agg ttc ctg tac acg ttc tat	241
Trp Ser Asp Asn Lys Ile Phe Arg Asp Arg Phe Leu Tyr Thr Phe Tyr	
65 70 75 80	
 ttc tgc tgc aga gaa ctg agg gag ttg ccg cca acg agt ttg gct gac	289
Phe Cys Cys Arg Glu Leu Arg Glu Leu Pro Pro Thr Ser Leu Ala Asp	
85 90 95	
 ttg att tcc aga gag tgg cct gac ccc gct gct cct ata aca gag atc	337
Leu Ile Ser Arg Glu Trp Pro Asp Pro Ala Ala Pro Ile Thr Glu Ile	
100 105 110	
 gtg tct caa ccg gag aga ctc ttg ttc gtc atc gac agc ttc gaa gag	385
Val Ser Gln Pro Glu Arg Leu Leu Phe Val Ile Asp Ser Phe Glu Glu	
115 120 125	
 ctg cag ggc ttg aac gaa ccc gat tcg gat ctg tgt ggt gac ttg	433
Leu Gln Gly Leu Asn Glu Pro Asp Ser Asp Leu Cys Gly Asp Leu	
130 135 140	
 atg gag aaa cgg ccg gtg cag gtg ctt ctg agc agt ttg ctg agg aag	481
Met Glu Lys Arg Pro Val Gln Val Leu Leu Ser Ser Leu Leu Arg Lys	
145 150 155 160	
 aag atg ctc ccg gag gcc tcc ctg ctc atc gct atc aaa ccc gtg tgc	529
Lys Met Leu Pro Glu Ala Ser Leu Leu Ile Ala Ile Lys Pro Val Cys	
165 170 175	
 ccg aag gag ctc cgg gat cag gtg acg atc tca gaa atc tac cag ccc	577
Pro Lys Glu Leu Arg Asp Gln Val Thr Ile Ser Glu Ile Tyr Gln Pro	
180 185 190	
 cg gga ttc aac gag agt gat agg tta gtg tat ttc tgc tgt ttc ttc	625
Arg Gly Phe Asn Glu Ser Asp Arg Leu Val Tyr Phe Cys Cys Phe Phe	
195 200 205	

Fig. 13A

aaa gac ccg aaa aga gcc atg gaa gcc ttc aat ctt gta aga gaa agt Lys Asp Pro Lys Arg Ala Met Glu Ala Phe Asn Leu Val Arg Glu Ser 210                   215                   220	673
gaa cag ctg ttt tcc ata tgc caa atc ccg ctc ctc tgc tgg atc ctg Glu Gln Leu Phe Ser Ile Cys Gln Ile Pro Leu Leu Cys Trp Ile Leu 225                   230                   235                   240	721
tgt acc agt ctg aag caa gag atg cag aaa gga aaa gac ctg gcc ctg Cys Thr Ser Leu Lys Gln Glu Met Gln Lys Gly Lys Asp Leu Ala Leu 245                   250                   255	769
acc tgc cag agc act acc tct gtg tac tcc tct ttc gtc ttt aac ctg Thr Cys Gln Ser Thr Ser Val Tyr Ser Ser Phe Val Phe Asn Leu 260                   265                   270	817
ttc aca cct gag ggt gcc gag ggc ccg act ccg caa acc cag cac cag Phe Thr Pro Glu Gly Ala Glu Gly Pro Thr Pro Gln Thr Gln His Gln 275                   280                   285	865
ctg aag gcc ctg tgc tcc ctg gct gca gag ggt atg tgg aca gac aca Leu Lys Ala Leu Cys Ser Leu Ala Ala Glu Gly Met Trp Thr Asp Thr 290                   295                   300	913
ttt gag ttt tgt gaa gac gac ctc cgg aga aat ggg gtt gtt gac gct Phe Glu Phe Cys Glu Asp Asp Leu Arg Arg Asn Gly Val Val Asp Ala 305                   310                   315                   320	961
gac atc cct gcg ctg ctg ggc acc aag ata ctt ctg aag tac ggg gag Asp Ile Pro Ala Leu Leu Gly Thr Lys Ile Leu Leu Lys Tyr Gly Glu 325                   330                   335	1009
cgt gag agc tcc tac gtg ttc ctc cac gtg tgt atc cag gag ttc tgt Arg Glu Ser Ser Tyr Val Phe Leu His Val Cys Ile Gln Glu Phe Cys 340                   345                   350	1057
gcc gcc ttg ttc tat ttg ctc aag agc cac ctt gat cat cct cac cca Ala Ala Leu Phe Tyr Leu Leu Lys Ser His Leu Asp His Pro His Pro 355                   360                   365	1105
gct gtg aga tgt gta cag gaa ttg cta gtt gcc aat ttt gaa aaa gca Ala Val Arg Cys Val Gln Glu Leu Leu Val Ala Asn Phe Glu Lys Ala 370                   375                   380	1153
agg aga gca cat tgg att ttt ttg ggg tgt ttt cta act ggc ctt tta Arg Arg Ala His Trp Ile Phe Leu Gly Cys Phe Leu Thr Gly Leu Leu 385                   390                   395                   400	1201
aat aaa aag gaa caa gaa aaa ctg gat gcg ttt ttt ggc ttc caa ctg Asn Lys Lys Glu Gln Glu Lys Leu Asp Ala Phe Phe Gly Phe Gln Leu 405                   410                   415	1249

Fig. 13B

tcc caa gag ata aag cag caa att cac cag tgc ctg aag agc tta ggg Ser Gln Glu Ile Lys Gln Gln Ile His Gln Cys Leu Lys Ser Leu Gly 420 425 430	1297
gag cgt ggc aat cct cag gga cag gtg gat tcc ttg gcg ata ttt tac Glu Arg Gly Asn Pro Gln Gly Gln Val Asp Ser Leu Ala Ile Phe Tyr 435 440 445	1345
tgt ctc ttt gaa atg cag gat cct gcc ttt gtg aag cag gca gtg aac Cys Leu Phe Glu Met Gln Asp Pro Ala Phe Val Lys Gln Ala Val Asn 450 455 460	1393
ctc ctc caa gaa gct aac ttt cat att att gac aac gtg gac ttg gtg Leu Leu Gln Glu Ala Asn Phe His Ile Ile Asp Asn Val Asp Leu Val 465 470 475 480	1441
gtt tct gcc tac tgc tta aaa tac tgc tcc agc ttg agg aaa ctc tgt Val Ser Ala Tyr Cys Leu Lys Tyr Cys Ser Ser Leu Arg Lys Leu Cys 485 490 495	1489
ttt tcc gtt caa aat gtc ttt aag aaa gag gat gaa cac agc tct acg Phe Ser Val Gln Asn Val Phe Lys Lys Glu Asp Glu His Ser Ser Thr 500 505 510	1537
tcg gat tac agc ctc atc tgt tgg cat cac atc tgc tct gtg ctc acc Ser Asp Tyr Ser Leu Ile Cys Trp His His Ile Cys Ser Val Leu Thr 515 520 525	1585
acc agc ggg cac ctc aga gag ctc cag gtg cag gac agc acc ctc agc Thr Ser Gly His Leu Arg Glu Leu Gln Val Gln Asp Ser Thr Leu Ser 530 535 540	1633
gag tcg acc ttt gtg acc tgg tgt aac cag ctg agg cat ccc agc tgt Glu Ser Thr Phe Val Thr Trp Cys Asn Gln Leu Arg His Pro Ser Cys 545 550 555 560	1681
cgc ctt cag aag ctt gga ata aat aac gtt tcc ttt tct ggc cag agt Arg Leu Gln Lys Leu Gly Ile Asn Asn Val Ser Phe Ser Gly Gln Ser 565 570 575	1729
gtt ctg ctc ttt gag gtg ctc ttt tat cag cca gac ttg aaa tac ctg Val Leu Leu Phe Glu Val Leu Phe Tyr Gln Pro Asp Leu Lys Tyr Leu 580 585 590	1777
agc ttc acc ctc acg aaa ctc tct cgt gat gac atc agg tcc ctc tgt Ser Phe Thr Leu Thr Lys Leu Ser Arg Asp Asp Ile Arg Ser Leu Cys 595 600 605	1825
gat gcc ttg aac tac cca gca ggc aac gtc aaa gag cta gcg ctg gta Asp Ala Leu Asn Tyr Pro Ala Gly Asn Val Lys Glu Leu Ala Leu Val 610 615 620	1873

Fig. 13C

aat tgt cac ctc tca ccc att gat tgt gaa gte ctt gct ggc ctt cta Asn Cys His Leu Ser Pro Ile Asp Cys Glu Val Leu Ala Gly Leu Leu 625	630	635	640	1921
acc aac aac aag aag ctg acg tat ctg aat gta tcc tgc aac cag tta Thr Asn Asn Lys Lys Leu Thr Tyr Leu Asn Val Ser Cys Asn Gln Leu 645	650		655	1969
gac aca ggc gtg ccc ctt ttg tgt gaa gcc ctg tgc agc cca gac acg Asp Thr Gly Val Pro Leu Leu Cys Glu Ala Leu Cys Ser Pro Asp Thr 660	665		670	2017
gtc ctg gta tac ctg atg ttg gct ttc tgc cac ctc agc gag cag tgc Val Leu Val Tyr Leu Met Leu Ala Phe Cys His Leu Ser Glu Gln Cys 675	680		685	2065
tgc gaa tac atc tct gaa atg ctt ctg cgt aac aag agc gtg cgc tat Cys Glu Tyr Ile Ser Glu Met Leu Leu Arg Asn Lys Ser Val Arg Tyr 690	695	700		2113
cta gac ctc agt gcc aat gtc ctg aag gac gaa gga ctg aaa act ctc Leu Asp Leu Ser Ala Asn Val Leu Lys Asp Glu Gly Leu Lys Thr Leu 705	710	715	720	2161
tgc gag gcc ttg aaa cat ccg gac tgc tgc ctg gat tca ctg tgt ttg Cys Glu Ala Leu Lys His Pro Asp Cys Cys Leu Asp Ser Leu Cys Leu 725	730		735	2209
gta aaa tgt ttt atc act gct gct ggc tgt gaa gac ctc gcc tct gct Val Lys Cys Phe Ile Thr Ala Ala Gly Cys Glu Asp Leu Ala Ser Ala 740	745		750	2257
ctc atc agc aat caa aac ctg aag att ctg caa att ggg tgc aat gaa Leu Ile Ser Asn Gln Asn Leu Lys Ile Leu Gln Ile Gly Cys Asn Glu 755	760		765	2305
atc gga gat gtg ggt gtg cag ctg ttg tgt cgg gct ctg acg cat acg Ile Gly Asp Val Gly Val Gln Leu Leu Cys Arg Ala Leu Thr His Thr 770	775	780		2353
gat tgc cgc tta gag att ctt ggg ttg gaa gaa tgt ggg tta acg agc Asp Cys Arg Leu Glu Ile Leu Gly Leu Glu Glu Cys Gly Leu Thr Ser 785	790	795	800	2401
acc tgc tgt aag gat ctc gcg tct gtt ctc acc tgc agt aag acc ctg Thr Cys Cys Lys Asp Leu Ala Ser Val Leu Thr Cys Ser Lys Thr Leu 805	810		815	2449
cag cag ctc aac ctg acc ttg aac acc ttg gac cac aca ggg gtg gtt Gln Gln Leu Asn Leu Thr Leu Asn Thr Leu Asp His Thr Gly Val Val 820	825		830	2497

Fig. 13 D

gta ctc tgt gag gcc ctg aga cac cca gag tgt gcc ctg cag gtg ctc      2545  
Val Leu Cys Glu Ala Leu Arg His Pro Glu Cys Ala Leu Gln Val Leu  
835                840                845

ggg gtt gtt gca gga gta aga acc aag cag      2575  
Gly Val Val Ala Gly Val Arg Thr Lys Gln  
850                855

Fig. 13E

Con  
Mol  
cut  
ins

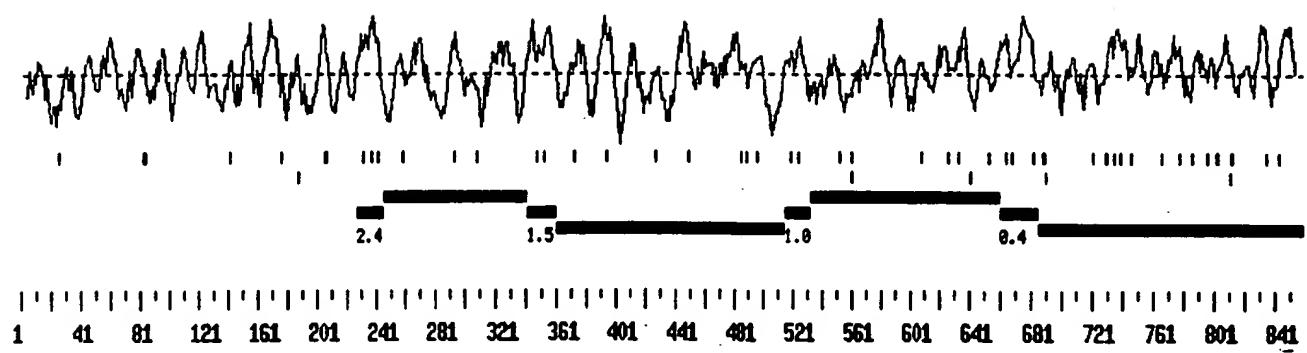


Fig. 14

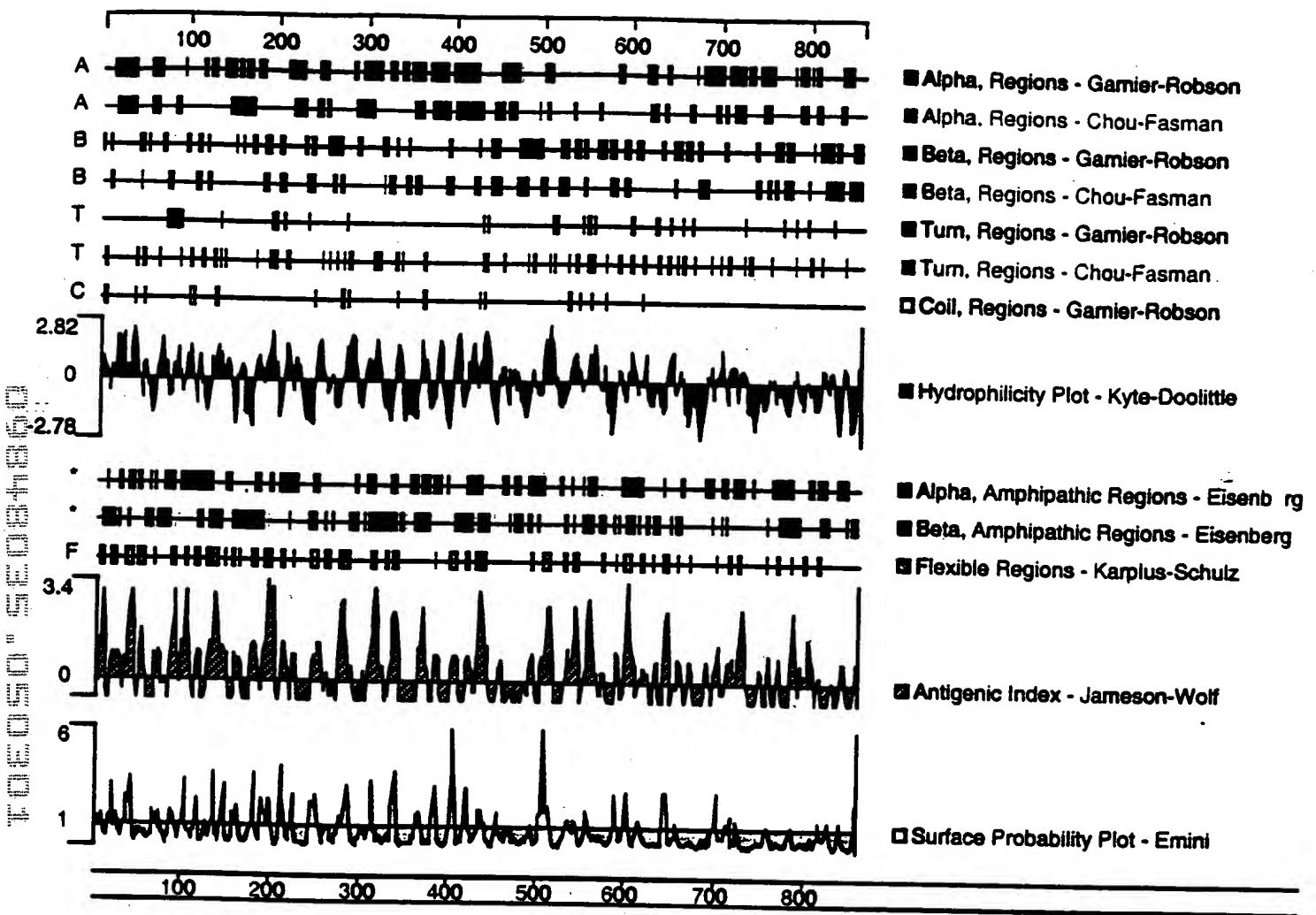


Fig. 15

LRR\_RI\_2: domain 1 of 8, from 530 to 557: score 6.4, E = 5.6  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
+ +LreL++++ + + ++ ++ L++  
NBS-5 530 SGHLRELQVQDSTLSESTFVTWCNQLRH 557

Fig. 16A

LRR\_RI\_2: domain 2 of 8, from 615 to 642: score 5.2, E = 8.4  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
+ +eL L n++l + + +La +L+  
NBS-5 615 AGNVKELALVNCHLSPIDCEVLAGLLTN 642

Fig. 16B

LRR\_RI\_2: domain 3 of 8, from 643 to 669: score 9.3, E = 2.2  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
n++L L++s+N 1 d G+ L+eaL s  
NBS-5 643 NKKLTLYLNVSCNQL-DTGVPLLCEALCS 669

Fig. 16C

LRR\_RI\_2: domain 4 of 8, from 699 to 726: score 32.8, E = 7.9e-06  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
n+s r LdLs N 1 deG + L+eaLk+  
NBS-5 699 NKSVRYLDLDSANVLKDEGLKTLCEALKH 726

Fig. 16 D

LRR\_RI\_2: domain 5 of 8, from 728 to 755: score 10.0, E = 1.8  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
++L L L + ++++G+ La+aL s  
NBS-5 728 DCCLDSCLVKCFITAAGCEDLASALIS 755

Fig. 16 E

LRR\_RI\_2: domain 6 of 8, from 756 to 783: score 30.9, E = 3e-05  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
n++L+ L+ ++++N +gd G++ L+ aL++  
NBS-5 756 NQNLKILQIGCNEIGDVGVQLLCRALTH 783

Fig. 16 F

LRR\_RI\_2: domain 7 of 8, from 785 to 812: score 8.0, E = 3.3  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
++L+ L L+ ++l+ ++ La++L+  
NBS-5 785 DCRLEILGLEECGLTSTCCKDLASVLTC 812

Fig. 16 G

LRR\_RI\_2: domain 8 of 8, from 813 to 840: score 17.6, E = 0.14  
SEQ ID NO:10 \*->npsLreLdLsnNklgdeGaraLaeaLks<-\*  
+++L+ L+L N+1 G+ +L+eaL++  
NBS-5 813 SKFLQQQLNLTNTLDHTGVVVLCLEARH 840

Fig. 16 H

Fig. 17A

gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser 225 230 235 240	778
atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp 245 250 255	826
gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp 260 265 270	874
tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys 275 280 285	922
agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg 290 295 300	970
gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac gta agg Ala Leu Arg Asp Leu Gln Leu Ala Gln Gln Pro Ile Tyr Val Arg 305 310 315 320	1018
gtg gag ggc ttc ctg gag gac agg agg gcc tat ttc ctg aga cac Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His 325 330 335	1066
ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser 340 345 350	1114
aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile 355 360 365	1162
gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccc gtc Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Val 370 375 380	1210
ccc acc tgc ctc acc cgc acg ggg ctg ttc ctg cgt ttc ctc tgc agc Pro Thr Cys Leu Thr Arg Thr Gly Leu Phe Leu Arg Phe Leu Cys Ser 385 390 395 400	1258
cgg ttc ccg cag ggc gca cag ctg cgg ggc gcg ctg cgg acg ctg agc Arg Phe Pro Gln Gly Ala Gln Leu Arg Gly Ala Leu Arg Thr Leu Ser 405 410 415	1306
ctc ctg gcc gcg cag ggc ctg tgg gcg cag atg tcc gtg ttc cac cga Leu Leu Ala Ala Gln Gly Leu Trp Ala Gln Met Ser Val Phe His Arg 420 425 430	1354
gag gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc Glu Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe 435 440 445	1402

Fig. 17B

ctg gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac Leu Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr 450 455 460	1450
tcc ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac Ser Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr 465 470 475 480	1498
gcc ctg gag aag gag gag ggg gag gac agg gac ggc cac gcc tgg gac Ala Leu Glu Lys Glu Glu Gly Glu Asp Arg Asp Gly His Ala Trp Asp 485 490 495	1546
atc ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac Ile Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn 500 505 510	1594
ccc gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag Pro Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu 515 520 525	1642
aag aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg Lys Arg Ala Lys Glu Leu Ala Thr Phe Gly Cys Arg Met Ser Pro 530 535 540	1690
gac atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat Asp Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn 545 550 555 560	1738
aag ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat Lys Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr 565 570 575	1786
gag tct cag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag Glu Ser Gln Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys 580 585 590	1834
gaa att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc Glu Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser 595 600 605	1882
ttc agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta Phe Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val 610 615 620	1930
gca aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att Ala Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile 625 630 635 640	1978
gaa ttt gaa agg tgc act tac cta acc att ccg aac tgg gct ccg cag Glu Phe Glu Arg Cys Thr Tyr Leu Thr Ile Pro Asn Trp Ala Arg Gln 645 650 655	2026
gat ctt cgc tct ctt cgc ctc tgg aca gat ttc tgc tct ctc ttc agc Asp Leu Arg Ser Leu Arg Leu Trp Thr Asp Phe Cys Ser Leu Phe Ser 660 665 670	2074

Fig. 17C

tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc ttc ctg agt Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser Phe Leu Ser 675                   680                   685	2122
gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt agc acc tgt Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg Ser Thr Cys 690                   695                   700	2170
cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac acc gcg tac His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp Thr Ala Tyr 705                   710                   715                   720	2218
cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc acg cac ctg Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu Thr His Leu 725                   730                   735	2266
acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg ctg atg ctg Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met Leu Met Leu 740                   745                   750	2314
tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac ctg agg ttg Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr Leu Arg Leu 755                   760                   765	2362
gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc ttc tat gtc Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe Phe Tyr Val 770                   775                   780	2410
ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca gcc aat gtg Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser Ala Asn Val 785                   790                   795                   800	2458
ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg aca cgc cca Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met Thr Arg Pro 805                   810                   815	2506
aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt ctt aca gaa Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg Leu Thr Glu 820                   825                   830	2554
gcc agt tgc aag gac ctt gct gtc ttg gtt gtc agc aag aag ctg Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser Lys Lys Leu 835                   840                   845	2602
aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca ggg gtg aag Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr Gly Val Lys 850                   855                   860	2650
ttt ctg tgt gag ggc ttg agt tac cct gat tgt aaa ctg cag acc ttg Phe Leu Cys Glu Gly Leu Ser Tyr Pro Asp Cys Lys Leu Gln Thr Leu 865                   870                   875                   880	2698
gtg tta cag caa tgc agc ata acc aag ctt ggc tgt aga tat ctc tca Val Leu Gln Gln Cys Ser Ile Thr Lys Leu Gly Cys Arg Tyr Leu Ser 885                   890                   895	2746

Fig. 17D

gag gcg ctc caa gaa gcc tgc agc ctc aca aac ctg gac ttg agt atc Glu Ala Leu Gln Glu Ala Cys Ser Leu Thr Asn Leu Asp Leu Ser Ile 900 905 910	2794
aac cag ata gct cgt gga ttg tgg att ctc tgt cag gca tta gag aat Asn Gln Ile Ala Arg Gly Leu Trp Ile Leu Cys Gln Ala Leu Glu Asn 915 920 925	2842
cca aac tgt aac cta aaa cac cta cggttg aag acc tat gaa act aat Pro Asn Cys Asn Leu Lys His Leu Arg Leu Lys Thr Tyr Glu Thr Asn 930 935 940	2890
ttg gaa atc aag aag ctgttg gag gaa gtg aaa gaa aag aat ccc aag Leu Glu Ile Lys Lys Leu Leu Glu Glu Val Lys Glu Lys Asn Pro Lys 945 950 955 960	2938
ctg act att gat tgc aat gct tcc ggg gca acg gca cct ccgtgc tgt Leu Thr Ile Asp Cys Asn Ala Ser Gly Ala Thr Ala Pro Pro Cys Cys 965 970 975	2986
gac ttt ttt tgc tgagcagcct gggatcgctc tacgaattac acaggaagcg Asp Phe Phe Cys 980	3038
ggattcgggt ctctaagatg tcttatgaat gcaggtcaga gggtcacatg ttaacactag agtctgtcga gagtaggat ttgacactgg tttctcaat tttttggaa gattctgcac gagtcacgca cccccttcac atgacgctat gtactttctc acaggataaa taaagttaga gcactctcaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaa	3098 3158 3218 3263

Fig. 17E

atg gca gaa tcg gat tct act gac ttt gac ctg ctg tgg tat cta gag Met Ala Glu Ser Asp Ser Thr Asp Phe Asp Leu Leu Trp Tyr Leu Glu	48
1                   5                   10                   15	
aat ctc agt gac aag gaa ttt cag agt ttt aag aag tat ctg gca cgc Asn Leu Ser Asp Lys Glu Phe Gln Ser Phe Lys Lys Tyr Leu Ala Arg	96
20                   25                   30	
aag att ctt gat ttc aaa ctg cca cag ttt cca ctg ata cag atg aca Lys Ile Leu Asp Phe Lys Leu Pro Gln Phe Pro Leu Ile Gln Met Thr	144
35                   40                   45	
aaa gaa gaa ctg gct aac gtg ttg cca atc tct tat gag gga cag tat Lys Glu Glu Leu Ala Asn Val Leu Pro Ile Ser Tyr Glu Gly Gln Tyr	192
50                   55                   60	
ata tgg aat atg ctc ttc agc ata ttt tca atg atg cgt aag gaa gat Ile Trp Asn Met Leu Phe Ser Ile Phe Ser Met Met Arg Lys Glu Asp	240
65                   70                   75                   80	
ctt tgt agg aag atc att ggc aga cga aac cat gtg ttc tac ata ctt Leu Cys Arg Lys Ile Ile Gly Arg Arg Asn His Val Phe Tyr Ile Leu	288
85                   90                   95	
caa tta gcc tat gat tct acc agc tat tat tca gca aac aat ctc aat Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu Asn	336
100                  105                  110	
gtg ttc ctg atg gga gag aga gca tct gga aaa act att gtt ata aat Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile Asn	384
115                  120                  125	
ctg gct gtg ttg agg tgg atc aag ggt gag atg tgg cag aac atg atc Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met Ile	432
130                  135                  140	
tcg tac gtc gtt cac ctc act tct cac gaa ata aac cag atg acc aac Ser Tyr Val Val His Leu Thr Ser His Glu Ile Asn Gln Met Thr Asn	480
145                  150                  155                  160	
agc agc ttg gct gag cta atc gcc aag gac tgg cct gac ggc cag gct Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln Ala	528
165                  170                  175	
ccc att gca gac atc ctg tct gat ccc aag aaa ctc ctt ttc att ctc Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile Leu	576
180                  185                  190	
gag gac ttg gac aac ata aga ttc gag tta aat gtc aat gaa agt gct Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser Ala	624
195                  200                  205	
ttg tgt agt aac agc acc cag aaa gtt ccc att cca gtt ctc ctg gtc Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu Val	672
210                  215                  220	

Fig. 18A

agt ttg ctg aag aga aaa atg gct cca ggc tgc tgg ttc ctc atc tcc	Ser Leu Leu Lys Arg Lys Met Ala Pro Gly Cys Trp Phe Leu Ile Ser	720	
225	230	235	240
tca agg ccc aca cgt ggg aat aat gta aaa acg ttc ttg aaa gag gta	Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu Val	768	
245	250	255	
gat tgc tgc acg acc ttg cag ctg tcg aat ggg aag agg gag ata tat	Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Ile Tyr	816	
260	265	270	
ttt aac tct ttc ttt aaa gac cgc cag agg gcg tcg gca gcc ctc cag	Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu Gln	864	
275	280	285	
ctt gta cat gag gat gaa ata ctc gtg ggt ctg tgc cga gtc gcc atc	Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala Ile	912	
290	295	300	
tta tgc tgg atc acg tgt act gtc ctg aag cgg cag atg gac aag ggg	Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys Gly	960	
305	310	315	320
cgt gac ttc cag ctc tgc tgc caa aca ccc act gat cta cat gcc cac	Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala His	1008	
325	330	335	
ttt ctt gct gat gcg ttg aca tca gag gct gga ctt act gcc aat cag	Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn Gln	1056	
340	345	350	
tat cac cta ggt ctc cta aaa cgt ctg tgt ttg ctg gct gca gga gga	Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly Gly	1104	
355	360	365	
ctg ttt ctg agc acc ctg aat ttc agt ggt gaa gac ctc aga tgt gtt	Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys Val	1152	
370	375	380	
ggg ttt act gag gct gat gtc tct gtg ttg cag gcc gcg aat att ctt	Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile Leu	1200	
385	390	395	400
ttg ccg agc aac act cat aaa gac cgt tac aag ttc ata cac ttg aac	Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu Asn	1248	
405	410	415	
gtc cag gag ttt tgt aca gcc att gca ttt ctg atg gca gta ccc aac	Val Gln Glu Phe Cys Thr Ala Ile Ala Phe Leu Met Ala Val Pro Asn	1296	
420	425	430	
tat ctg atc ccc tca ggc agc aga gag tat aaa gag aag aga gaa caa	Tyr Leu Ile Pro Ser Gly Ser Arg Glu Tyr Lys Glu Lys Arg Glu Gln	1344	
435	440	445	

Fig. 18B

tac tct gac ttt aat caa gtg ttt act ttc att ttt ggt ctt cta aat Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu Asn 450 455 460	1392
gca aac agg aga aag att ctt gag aca tcc ttt gga tac cag cta ccg Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu Pro 465 470 475 480	1440
atg gta gac agc ttc aag tgg tac tcg gtg gga tac atg aaa cat ttg Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His Leu 485 490 495	1488
gac cgt gac ccg gaa aag ttg acg cac cat atg cct ttg ttt tac tgt Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr Cys 500 505 510	1536
ctc tat gag aat cgg gaa gaa gaa ttt gtg aag acg att gtg gat gct Leu Tyr Glu Asn Arg Glu Glu Phe Val Lys Thr Ile Val Asp Ala 515 520 525	1584
ctc atg gag gtt aca gtt tac ctt caa tca gac aag gat atg atg gtc Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met Val 530 535 540	1632
tca tta tac tgt ctg gat tac tgc tgt cac ctg agg aca ctt aag ttg Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys Leu 545 550 555 560	1680
agt gtt cag cgc atc ttt caa aac aaa gag cca ctt ata agg cca act Ser Val Gln Arg Ile Phe Gln Asn Lys Glu Pro Leu Ile Arg Pro Thr 565 570 575	1728
gct agt caa atg aag agc ctt gtc tac tgg aga gag atc tgc tct ctt Ala Ser Gln Met Lys Ser Leu Val Tyr Trp Arg Glu Ile Cys Ser Leu 580 585 590	1776
ttt tat aca atg gag agc ctc cgg gag ctg cat atc ttt gac aat gac Phe Tyr Thr Met Glu Ser Leu Arg Glu Leu His Ile Phe Asp Asn Asp 595 600 605	1824
ctt aat ggt att tca gaa agg att ctg tct aaa gcc ctg gag cat tct Leu Asn Gly Ile Ser Glu Arg Ile Leu Ser Lys Ala Leu Glu His Ser 610 615 620	1872
agc tgt aaa ctt cgc aca ctc aag ttg tcc tat gtc tcg act gct tct Ser Cys Lys Leu Arg Thr Leu Lys Leu Ser Tyr Val Ser Thr Ala Ser 625 630 635 640	1920
ggg ttt gaa gac tta ctc aag gct ttg gct cgt aat cgg agc ctg aca Gly Phe Glu Asp Leu Leu Lys Ala Leu Ala Arg Asn Arg Ser Leu Thr 645 650 655	1968
tac ctg agt atc aac tgt acg tcc att tcc cta aat atg ttt tca ctt Tyr Leu Ser Ile Asn Cys Thr Ser Ile Ser Leu Asn Met Phe Ser Leu 660 665 670	2016

Fig. 18C

ctg cat gac atc ctg cac gag ccc aca tgc caa ata agt cat ctg agc Leu His Asp Ile Leu His Glu Pro Thr Cys Gln Ile Ser His Leu Ser 675                   680                   685	2064
ttg atg aaa tgt gat ttg cga gcc agc gaa tgc gaa gaa atc gcc tct Leu Met Lys Cys Asp Leu Arg Ala Ser Glu Cys Glu Glu Ile Ala Ser 690                   695                   700	2112
ctc ctc atc agt ggc ggg agt ctg aga aaa ctg acc tta tcc agc aat Leu Leu Ile Ser Gly Gly Ser Leu Arg Lys Leu Thr Leu Ser Ser Asn 705                   710                   715                   720	2160
ccg ctg agg agc gac ggg atg aac ata ctg tgt gat gcc ttg ctt cat Pro Leu Arg Ser Asp Gly Met Asn Ile Leu Cys Asp Ala Leu Leu His 725                   730                   735	2208
ccc aac tgc act ctt ata tca ctg gtt ctg tct ggc tgt ttc ttt agc Pro Asn Cys Thr Leu Ile Ser Leu Val Leu Ser Gly Cys Phe Phe Ser 740                   745                   750	2256
agc gat atc tgtcaa tat att gcc ata gtt att gct act aat gaa aaa Ser Asp Ile Cys Gln Tyr Ile Ala Ile Val Ile Ala Thr Asn Glu Lys 755                   760                   765	2304
ctg agg agc ctg gag att ggg agc aac aaa ata gaa gat gca gga atg Leu Arg Ser Leu Glu Ile Gly Ser Asn Lys Ile Glu Asp Ala Gly Met 770                   775                   780	2352
cag ctg cta tgt ggt ttg aga cat ccc aac tgc atg ttg gtg aat Gln Leu Leu Cys Gly Gly Leu Arg His Pro Asn Cys Met Leu Val Asn 785                   790                   795                   800	2400
att ggg cta gaa gag tgc atg tta acc agt gcc tgc tgt cga tct ctt Ile Gly Leu Glu Glu Cys Met Leu Thr Ser Ala Cys Cys Arg Ser Leu 805                   810                   815	2448
gcc tct gtt ctt acc acc aac aaa aca cta gaa aga ctc aac ttg ctt Ala Ser Val Leu Thr Thr Asn Lys Thr Leu Glu Arg Leu Asn Leu Leu 820                   825                   830	2496
caa aat cac ttg ggc aat gat gga gtt gca aaa ctt ctt gag agc ttg Gln Asn His Leu Gly Asn Asp Gly Val Ala Lys Leu Leu Glu Ser Leu 835                   840                   845	2544
atc agc cca gat tgt gta ctt aag gta gtt ggc ttg atg gct gct gag Ile Ser Pro Asp Cys Val Leu Lys Val Val Gly Leu Met Ala Ala Glu 850                   855                   860	2592
aac atg gag tcc ctc att ccc agg cca gca cgc tga Asn Met Glu Ser Leu Ile Pro Arg Pro Ala Arg 865                   870                   875	2628

Fig. 18D